

## CLAIMS

What Is Claimed Is:

- 1 1. A method comprising:
  - 2 predicting a secondary structure of a protein;
  - 3 superimposing the predicted secondary structure on a set of topomers;
  - 4 refining the superimposed secondary structure; and
  - 5 predicting a tertiary structure of a protein
- 1 2. The method of claim 1, wherein said secondary structure is a consensus  
2 secondary structure prediction.
- 1 3. The method of claim 1, further comprising annealing the secondary structure by  
2 energy minimization.
- 1 4. The method of claim 3, wherein said energy minimization is by a random  
2 Monte Carlo method.
- 1 5. The method of claim 4, wherein the random Monte Carlo method uses random  
2 moves from a log probability table.
- 1 6. The method of claim 3, wherein the random Monte Carlo method uses smart  
2 moves.
- 1 7. The method of claim 1, wherein the secondary structure superimposed on a set  
2 of topomers is refined by energy minimization.
- 1 8. The method of claim 7, wherein the secondary structure superimposed on a set  
2 of topomers is refined using a molecular modeling program.
- 1 9. The method of claim 8, wherein the molecular modeling program is X-PLOR.
- 1 10. A method comprising:
  - 2 predicting a secondary structure of a protein;
  - 3 generating a three-dimensional representation of the predicted secondary structure;

4 optimizing the secondary structure by adjusting dihedral angles using smart moves; and  
5 determining a three-dimensional protein structure by modeling the optimized secondary  
6 structure on a topomer model.

1 11. The method of claim 10, wherein said secondary structure is a consensus  
2 secondary structure prediction.

1 12. The method of claim 10, wherein optimization is performed using a random  
2 Monte Carlo method.

1 13. The method of claim 12, wherein the random Monte Carlo method is used in  
2 conjunction with a localized energy function.

1 14. The method of claim 10, wherein said three-dimensional structure model is  
2 refined using simulated annealing.

1 15. A machine readable medium that provides instructions, which when executed  
2 by a machine cause said machine to perform a method comprising:  
3 predicting a secondary structure of protein;  
4 superimposing the secondary structure on a topomer model; and  
5 refining the topomer model.

1 16. A machine readable medium as in claim 15, wherein said secondary structure is  
2 a consensus secondary structure prediction.

1 17. A machine readable medium as in claim 15, further comprising energy  
2 minimization of the secondary structure prediction.

1 18. A machine readable medium as in claim 17, wherein said energy minimization  
2 is by a random Monte Carlo method.

1 19. A machine readable medium as in claim 18, wherein random moves are selected  
2 from a log probability table.

1 20. A machine readable medium as in claim 15, wherein the topomer model is  
2 refined by topological entropy minimization.

1 21. A machine readable medium as in claim 20, wherein the topomer model is  
2 refined by a molecular modeling program.